The specification has been amended to include the Sequence Listing submitted herewith on separate sheets. It has been noted that the Sequence Listing filed on October 15, 2001 numbered the sequences differently to the specification. The new Sequence Listing differs from the old Sequence Listing only in the order in which the sequences are presented. The numbering of the sequences in the new Listing corresponds to the SEQ ID numbers given in the specification. Entry of the Sequence Listing does not raise the issue of new matter as the sequence information contained therein is presented in the application as originally filed. The computer readable copy of the Sequence Listing submitted herewith is the same as the attached paper copy of that Listing.

Reconsideration of the restriction requirement is requested in view of the above-noted claim amendments and further in view of the comments that follow.

The claims have been amended to specify that the second polypeptide is a human papillomavirus (HPV) polypeptide. Applicants submit that the foregoing amendments address the Examiner's concerns.

Neither of the documents cited by the Examiner discloses, nor would either have suggested, a method according to the amended claims wherein the first polypeptide comprises a sequence consisting essentially of the sequence of SEQ ID NO:1 and wherein the second polypeptide is an HPV polypeptide. Applicants therefore submit that the claimed subject matter is novel.

The citations upon which the Examiner relies provide no evidence that would have suggested that an interaction between a polypeptide comprising the sequence of SEQ ID NO: 1 and an HPV polypeptide might exist. There would, therefore, have been no motivation to

conduct a method according to the invention to determine whether a candidate compound was capable of disrupting the interaction between such a "TRAM" polypeptide and an HPV polypeptide.

Applicants submit that this amendment to Groups I and II defined by the Examiner means that the resulting invention provides a clear contribution over the art. Applicants submit that Groups I and II as amended are therefore linked by a special technical feature and form a single general inventive concept under PCT Rule 13.1. The claims of Groups III and IV have been deleted.

If, in spite of the above, the Examiner is inclined to maintain the restriction requirement, Applicants elect Group I as determined by the Examiner, and as specified in claims 36 to 44 and 52 to 57.

The Examiner has further indicated that the TRIM sequence of the claims should be defined with reference to a specific sequence identification number. Applicants submit that the amendment to specify that the second polypeptide is an HPV polypeptide which binds to the TRAM sequence should be sufficient and request reconsideration. Applicants recognize that this amendment encompasses more than one specific sequence, but submit that it would be unduly limiting to require restriction to a specific sequence from a particular HPV strain. It is submitted that the invention pertains to more than one HPV strain, and that different strains may bind to SEQ ID NO: 1 via slightly different amino acid sequences.

However, if the Examiner is inclined to maintain this requirement, Applicants request that the definition of the TRIM sequence in the claims be restricted to HPV E6 protein as specified in claim 40 or, if the Examiner maintains the requirement for a specified amino acid

sequence, to the sequence of amino acids 100 to 147 of HPV-16 E6 as shown in Figure 9a, and as specified in new claim 57.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached pages are captioned "Version With Markings To Show Changes Made."

An early and favorable Action is requested.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE CLAIMS:

36. (Amended) A method for determining whether a compound is capable of inhibiting or disrupting an interaction between a first polypeptide and a second polypeptide said method comprising:

(a) (i) incubating said first polypeptide with said second polypeptide under conditions which allow the first polypeptide to bind to the second polypeptide to form a complex; and bringing the complex thus formed into contact with a candidate compound; or

(ii) incubating said first polypeptide with said second polypeptide in the presence of a candidate compound under conditions which would allow the first polypeptide to bind to the second polypeptide in the absence of the candidate compound; and

(b) determining if said candidate compound inhibits or disrupts binding of the first polypeptide to the second polypeptide;

wherein said first polypeptide comprises a TRAM sequence consisting essentially of the sequence show in in SEQ ID NO:1 and said second polypeptide is a human papillomavirus (HPV) polypeptide comprising (~~comprises~~) a TRIM sequence which binds to a said TRAM sequence.

40. (Amended) The method according to claim 36 ~~(39)~~ wherein said HPV polypeptide is E6.

41. (Amended) The method according to claim 36 wherein said first polypeptide ~~(and/or said second polypeptide)~~ is a polypeptide found in eukaryotic cells.

43. (Amended) The method according to claim 41 wherein said eukaryotic polypeptide is selected from mdm2, (~~p53, TBP, E2F, YY,~~) CBP, and p300, (~~MyoD and TFIIB~~).

45. (Amended) A method for identifying a compound which interacts with a polypeptide comprising a TRAM sequence consisting essentially of the sequence shown in SEQ ID NO:1 and/or a HPV polypeptide comprising a TRIM sequence which binds to a said TRAM sequence, which method comprises:

(a) incubating a candidate compound with a polypeptide comprising a TRAM sequence and/or TRIM sequence under suitable conditions; and

(b) determining if said candidate compound interacts with said polypeptide comprising a TRAM sequence and/or a TRIM sequence.